

Raw Sequence Listing Error Summary

ERROR DETECTED SUGGESTED CORRECTION

SERIAL NUMBER: 09/602,874

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

- 1 Wrapped Nucleics The number/text at the end of each line "wrapped" down to the next line.
This may occur if your file was retrieved in a word processor after creating it.
Please adjust your right margin to .3, as this will prevent "wrapping".
- 2 Wrapped Aminos The amino acid number/text at the end of each line "wrapped" down to the next line.
This may occur if your file was retrieved in a word processor after creating it.
Please adjust your right margin to .3, as this will prevent "wrapping".
- 3 Incorrect Line Length The rules require that a line not exceed 72 characters in length. This includes spaces.
- 4 Misaligned Amino Acid Numbering The numbering under each 5th amino acid is misaligned. This may be caused by the use of tabs between the numbering. It is recommended to delete any tabs and use spacing between the numbers.
- 5 Non-ASCII This file was not saved in ASCII (DOS) text, as required by the Sequence Rules.
Please ensure your subsequent submission is saved in ASCII text so that it can be processed.
- 6 Variable Length Sequence(s) contain n's or Xaa's which represented more than one residue.
As per the rules, each n or Xaa can only represent a single residue.
Please present the maximum number of each residue having variable length and indicate in the (ix) feature section that some may be missing.
- 7 PatentIn ver. 2.0 "bug" A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequence(s) . Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence.
- 8 Skipped Sequences (OLD RULES) Sequence(s) missing. If intentional, please use the following format for each skipped sequence:
(2) INFORMATION FOR SEQ ID NO:X:
(i) SEQUENCE CHARACTERISTICS:(Do not insert any headings under "SEQUENCE CHARACTERISTICS")
(xi) SEQUENCE DESCRIPTION:SEQ ID NO:X:
This sequence is intentionally skipped

Please also adjust the "(iii) NUMBER OF SEQUENCES:" response to include the skipped sequence(s).
- 9 Skipped Sequences (NEW RULES) Sequence(s) missing. If intentional, please use the following format for each skipped sequence.
<210> sequence id number
<400> sequence id number
000
- 10 Use of n's or Xaa's (NEW RULES) Use of n's and/or Xaa's have been detected in the Sequence Listing.
Use of <220> to <223> is MANDATORY if n's or Xaa's are present.
In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.
- 11 Use of <213>Organism (NEW RULES) Sequence(s) are missing this mandatory field or its response.
- 12 Use of <220>Feature (NEW RULES) Sequence(s) are missing the <220>Feature and associated headings.
Use of <220> to <223> is MANDATORY if <213>ORGANISM is "Artificial" or "Unknown"
Please explain source of genetic material in <220> to <223> section.
(See "Federal Register," 6/01/98, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of new Rules)
- 13 PatentIn ver. 2.0 "bug" Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing).
Instead, please use "File Manager" or any other means to copy file to floppy disk.

RAW SEQUENCE LISTING

DATE: 07/07/2000

PATENT APPLICATION: US/09/602,874

TIME: 13:17:48

Input Set : A:\seqlist.txt

Output Set: N:\CRF3\07072000\I602874.raw

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8696      210      215      220
8698 Leu Thr His Ala Leu Asn Gln Trp Lys Asn Thr Ile Thr Ser Ala Ser
8699 225      230      235      240
8701 Leu Gln Leu Val Ile Leu Val Glu Glu Pro Pro Ala Glu Ser Asp Tyr
8702      245      250      255
8704 Glu Asp Pro Met Asp Ser Val Trp Pro Val Arg Leu Met Val Arg Thr
8705      260      265      270
8707 Gly Val Asp Ala Pro Gln Ala Ile Gln Lys Gly Ser Ile Asp Ser Gly
8708      275      280      285
8710 Gly Met Glu Gln Leu Arg Ser Gln Tyr Glu Thr Ala Lys Thr Thr Ser
8711      290      295      300
8713 Met Leu Leu Asp Pro Ala Arg Glu Asp Ala Met Leu Gly His Met Val
8714 305      310      315      320
8716 Asp Ile Ala Gln Asn Gly Asp Trp Asp Ile Phe Leu Thr Thr Glu Glu
8717      325      330      335
8719 Ile Val Asn Phe Ile Ser His Asp Val Ala Lys Leu Arg Lys Ala Gly
8720      340      345      350
8722 Ile Pro Val Met Leu Pro Lys Ala Trp Ser Thr Tyr Glu Thr Arg Ala
8723      355      360      365
8725 Gln Val Glu Ala Arg Thr Pro Asn Asp Ala Ala Asp Ser Ser Thr Lys
8726      370      375      380
8728 Ala Ile Ile Gly Leu Asp Gln Leu Val Glu Tyr Asn Trp Arg Ile Ser
8729 385      390      395      400
8731 Val Gly Asp Ile Gln Leu Ser Asp Glu Glu Met Arg Glu Leu Ile Asp
8732      405      410      415
8734 Ser Lys Thr Gly Leu Ile Arg Leu Arg Gly Asp Trp Val Met Ala Asp
8735      420      425      430
8737 Gln Asp Ala Leu Arg Arg Ile Thr Ser Tyr Met Glu Glu Leu Ser Lys
8738      435      440      445
8740 Ser Ser Glu Lys Arg Ala Arg Thr Glu Met Glu Lys Val Ala Met Gln
8741      450      455      460
8743 Ala Lys Leu Ala Glu Ala Asn Gly Glu Glu Gly Trp Gln Leu Leu Ala
8744 465      470      475      480
8746 Ala Lys Ala Glu Thr Leu Arg Lys Glu Phe Asn Glu Lys Phe Ser Gly
8747      485      490      495
8749 Asp Gly Gln Gly Glu Val Thr Leu Ala Glu Leu Arg Glu Ile Ala Leu
8750      500      505      510
8752 Lys Ala Ala Glu Asn Glu Pro Val Glu Phe Thr Gly Ser Gln Trp Phe
8753      515      520      525
8755 Asn Ser Leu Leu Gly Gly Thr Glu Thr Pro Ala Pro Val Arg Val Asp
8756      530      535      540
8758 Ile Pro Asp Thr Val Leu Ala Asp Leu Arg Glu Tyr Gln Arg Arg Gly
8759 545      550      555      560
8761 Val Asp Trp Leu Tyr Trp Met Ser Ala Asn Asn Leu Gly Ala Val Leu
8762      565      570      575
8764 Ala Asp Asp Met Gly Leu Gly Lys Thr Leu Gln Leu Leu Ser Leu Leu
8765      580      585      590
8767 Ala Val Glu Arg Ala Glu Asn Pro Glu Leu Glu Arg Gly Pro Thr Leu
8768      595      600      605

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8770 Val Val Cys Pro Thr Ser Val Val Gly Asn Trp Ala Ala Glu Ala Ala
8771      610      615      620
8773 Lys Phe Val Pro Ser Leu Lys Val Leu Met His His Gly Pro Gln Arg
8774 625      630      635      640
8776 Leu Asn Asp Ala Asp Phe Leu Ser Gln Ser Lys Gly Met Asp Leu Ile
8777      645      650      655
8779 Ile Thr Ser Tyr Gly Val Ile Thr Arg Asp Phe Lys Leu Met Gly Gln
8780      660      665      670
8782 Val Gly Phe Glu Arg Val Val Leu Asp Glu Ala Gln Ala Ile Lys Asn
8783      675      680      685
8785 Ser Ser Thr Arg Val Ser Lys Ala Val Arg Ser Leu Pro Ser Arg His
8786      690      695      700
8788 Arg Val Ala Leu Thr Gly Thr Pro Val Glu Asn Arg Leu Ser Glu Met
8789 705      710      715      720
8791 Arg Ser Ile Leu Asp Phe Cys Asn Pro Gly Val Leu Gly Ser Ala Ser
8792      725      730      735
8794 Phe Phe Arg Asn His Phe Ala Lys Ala Ile Glu Arg Glu Gln Asp Asp
8795      740      745      750
8797 Thr Met Thr Glu Arg Leu Arg Gln Leu Thr Ala Pro Phe Ile Leu Arg
8798      755      760      765
8800 Arg Leu Lys Thr Asp Pro Asn Ile Ile Asp Asp Leu Pro Glu Lys Thr
8801      770      775      780
8803 Glu Gln Ile Ile Arg Val Asp Met Thr Thr Glu Gln Ala Ser Leu Tyr
8804 785      790      795      800
8806 Lys Ala Leu Val Glu Asp Val Gln Lys Gln Leu Asp Glu Arg Gln Gly
8807      805      810      815
8809 Met Ser Arg Lys Gly Leu Val Leu Ala Thr Ile Thr Arg Ile Lys Gln
8810      820      825      830
8812 Ile Cys Asn His Pro Ala His Phe Leu Gly Asp Gly Ser Glu Val Thr
8813      835      840      845
8815 Leu Lys Gly Lys His Arg Ser Gly Lys Val Glu Ala Leu Met Glu Leu
8816      850      855      860
8818 Ile Asp Thr Ala Val Lys Glu Glu Arg Arg Met Leu Ile Phe Thr Gln
8819 865      870      875      880
8821 Tyr Ala Ala Phe Gly Arg Ile Leu Ala Pro Tyr Leu Ser Asp Arg Leu
8822      885      890      895
8824 Gly Thr Asn Ile Pro Phe Leu His Gly Gly Val Thr Lys Pro Gly Arg
8825      900      905      910
8827 Asp Arg Met Val Ala Glu Phe Gln Ser Glu Asp Gly Pro Pro Ala Met
8828      915      920      925
8830 Ile Leu Ser Leu Lys Ala Gly Gly Thr Gly Leu Asn Leu Thr Ala Ala
8831      930      935      940
8833 Ser Ile Val Val His Met Asp Arg Trp Trp Asn Pro Ala Val Glu Asn
8834 945      950      955      960
8836 Gln Ala Thr Asp Arg Ala Phe Arg Ile Gly Gln Arg Lys Asn Val Asp
8837      965      970      975
8839 Val Tyr Lys Met Ile Thr Val Gly Thr Met Glu Glu Ser Ile Gln Asp
8840      980      985      990
8842 Ile Leu Asp Gly Lys Thr His Leu Ala Ser Ala Ile Val Gly Glu Gly

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E--> 8843 995 1000 1005
 8845 Glu Gly Trp Ile Thr Glu Leu Asn Pro Glu Glu Leu Ala Met Leu Met
 E--> 8846 1010 1015 1020
 8848 Ser Tyr Arg Glu Lys Glu Gly Ala Asp Asp
 8849 1025 1030
 20670 <210> SEQ ID NO: 284
 20671 <211> LENGTH: 1124
 20672 <212> TYPE: PRT
 20673 <213> ORGANISM: Corynebacterium glutamicum
 20675 <400> SEQUENCE: 284
 20676 Met Pro Ala Gly Ile Ala Asp Met Thr Asp Ser Leu Leu Gly Trp Ala
 20677 1 5 10 15
 20679 Ser Gln Thr Glu Leu Asp Leu Asn Gln Arg Leu Ala Gly Val Glu Tyr
 20680 20 25 30
 20682 Phe Pro Gln Ile Gln Leu Arg His Asp Glu Leu Glu Arg Ile His Arg
 20683 35 40 45
 20685 Phe Tyr Gly Thr Phe Leu Ser Arg Gln Val Gly Ala Gly Ala Ser Leu
 20686 50 55 60
 20688 Gly Asp Leu Phe Glu Met Thr Pro Cys Leu Thr Val Thr Thr Leu Val
 20689 65 70 75 80
 20691 Ser Arg Ala Ser Arg Ile Ser Asp Pro Ala Asp Phe Phe Gly Glu Tyr
 20692 85 90 95
 20694 Ile Gly Gly Leu Gly Leu Ser Ala Glu His Ala Ala Val Val Glu Gly
 20695 100 105 110
 20697 Leu Thr Glu Lys Leu Phe Ala Gln Ala Gly Leu Leu Val Pro Glu Gly
 20698 115 120 125
 20700 Ile Ala Ser Pro Leu Glu Leu Leu Ser Ile His Ala Gly Ile Ser Asn
 20701 130 135 140
 20703 His Glu Val Ala Ala Val Leu Thr Glu Val Glu Asn Gly Thr Thr Glu
 20704 145 150 155 160
 20706 Tyr Pro Phe Met Phe Asp Ala Val Leu Arg Leu Thr Pro Glu Trp Ala
 20707 165 170 175
 20709 Gln Thr Leu Ile Gly Gly Val Gln Glu Leu Ile Glu Phe Ala Thr Thr
 20710 180 185 190
 20712 His Arg Thr Ser Trp Ser Asp Arg Gln Arg Glu Ser Ser Leu Pro Ala
 20713 195 200 205
 20715 Met Ile Asp Glu Ile Val Val Ala Glu Leu Arg Glu Arg Pro Val Gly
 20716 210 215 220
 20718 Thr Ala Asp Arg Glu Asn Ser Val Gly Val Ala Leu Arg Glu Leu Arg
 20719 225 230 235 240
 20721 Pro Arg Leu Ile Leu Asp Ala Glu Arg Arg Lys Val Cys Leu Arg Leu
 20722 245 250 255
 20724 Pro Glu Gln Arg Val Ser Asp Asp Glu Ile Asn Trp Arg Val Ser Leu
 20725 260 265 270
 20727 Glu Gly Thr Thr Arg Ile Phe Ser Thr Arg Arg Ala Trp Gly Asp Thr
 20728 275 280 285
 20730 Ser Gly Tyr Ser Glu Ala Leu Asp Ile Thr Val Glu Arg Gln Ile Arg
 20731 290 295 300
 20733 Glu Thr Thr Val Thr Asp Thr Ser Asn Gln Ile Thr Trp Val Val Pro

*misaligned numbering - see
 idea of*

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*in Error
 summary sheet*

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Output Set: N:\CRF3\07072000\I602874.raw

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20734 305          310          315          320
20736 Val Val Asp Phe Asn Asp Pro Val Leu Val Phe Ser Ala Arg Gly Glu
20737          325          330          335
20739 Asn Leu Thr Asp Lys Val Ser Leu His Gln Glu Ile Tyr Val Leu
20740          340          345          350
20742 Ala Pro Ala Glu Ala Lys Leu Glu Asp Met Val Thr Gly Gln Pro Val
20743          355          360          365
20745 Pro Val Ile Glu Gln Phe Leu Val Glu Gly Trp Asn Ser Trp Val Cys
20746          370          375          380
20748 Ser Arg Val Asp Ala Arg Gly Leu Ser Ser Leu Lys Val Asn Lys Glu
20749 385          390          395          400
20751 Val Arg Cys Ile Asp Pro Arg Arg Arg Val Ala Phe His His Pro Ala
20752          405          410          415
20754 Glu Leu Val Pro His Val Arg Ser Ile Ser Gly Leu Pro Val His Ala
20755          420          425          430
20757 Gln Ser Leu Ile Ala Glu Phe Pro Pro Thr Leu Ser Gly Gln Asp Glu
20758          435          440          445
20760 Thr Trp Met Leu Ser Ile Ser Ala Phe Ala Gly Val Gly Ala Ala Gly
20761          450          455          460
20763 Glu Glu Ile Ala Glu Pro Glu Pro Leu Glu Val Pro Ala Asp Gly Gly
20764 465          470          475          480
20766 Leu Phe Ala Ile Phe Asp Pro Glu Ile Tyr Asp Ala Pro Trp Val Gly
20767          485          490          495
20769 Glu Tyr Leu Val Arg Leu Arg Gly Pro Arg Asn Glu Ser Phe Arg Pro
20770          500          505          510
20772 Glu Phe Ala Ile Val Glu Asp Met Thr Thr Glu Phe Glu Val Ala Ser
20773          515          520          525
20775 Gly Ala Ser Phe Arg Ile Pro Thr Thr Thr Gly Leu Ser Glu Ala Ser
20776          530          535          540
20778 Leu Arg Val Arg Ser Gly Glu Lys His Phe Thr Ala Glu Pro Arg Leu
20779 545          550          555          560
20781 Val Thr Val Glu Ala Thr Asp Pro Asn Ala Ser Phe Val Val Thr Thr
20782          565          570          575
20784 Asp Glu Gly Asp Gln Met Pro Leu Arg Phe Val Pro Pro Gln Ile Ala
20785          580          585          590
20787 Ile Glu Leu Pro Leu Thr Thr Glu Pro Pro Thr Trp Arg Val Thr Arg
20788          595          600          605
20790 Thr Val Cys Gly Pro Arg Asp Leu Asp Gly Ala Gly Glu Leu Arg Ile
20791          610          615          620
20793 Arg Thr Gly Val Asp Val Gly Asp Pro Lys Val Ser Val Arg Asn His
20794 625          630          635          640
20796 His Gly Ser Pro Leu Arg Thr Val Lys Met Val Thr Pro Asp Asn Gly
20797          645          650          655
20799 Arg Thr Trp Ile Ala Ser Met Lys Glu Ile Ala Ala Ser Thr Phe Val
20800          660          665          670
20802 Met Pro Arg Gly Ser Ile Glu Phe Glu Trp Thr Asp Arg Lys Val Asp
20803          675          680          685
20805 Arg Arg Val Ser Val Thr Ile Ala Val Ile Asp Lys Thr Glu Asn Phe
20806          690          695          700

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20808 Thr Gly Ile Thr Ile Glu Asp Gly Lys Leu Val Phe Glu Glu Leu Ala
20809 705 710 715 720
20811 Ala Gly Arg Gln Leu Ala Ala Trp Val Trp Pro Gln Thr Ala Pro Trp
20812 725 730 735
20814 Val Ser Ala Val Glu Leu Ala Val Thr Gly Pro Glu Leu Glu Leu Pro
20815 740 745 750
20817 Glu Val Leu Val Gly Ala Gly Asn Leu Ile Val Gln Leu His Thr Ala
20818 755 760 765
20820 Asp Pro Phe Thr Thr Ser Val Thr Pro Leu Ser Pro Gly Lys Ala Ala
20821 770 775 780
20823 Val Thr Val Glu Gln Glu Gly Tyr Tyr Ser Ala Gln Thr Glu Glu Tyr
20824 785 790 795 800
20826 Ala Gln Leu Ser Ala Phe Phe Gly Gly Glu Val Glu Glu Pro Pro Ile
20827 805 810 815
20829 Ser Asp Ala Val Val Pro Ala Leu Trp Asp Val Ser His Ile Trp Thr
20830 820 825 830
20832 Glu Gln Gly Asn Thr Glu His Leu Pro Val Val His Ala Ala Leu Arg
20833 835 840 845
20835 Ser Ser Pro Ala Ala Ala Leu Lys Gly Leu Ser Ala Ser Leu Val Pro
20836 850 855 860
20838 Ala Gln Ala Leu Pro Gly Lys Val Ile Ser Ser Gly Leu Ala Ala Ser
20839 865 870 875 880
20841 Pro Phe Thr Thr Glu Ser Pro Ala Thr Glu Val His Arg Thr Ala Trp
20842 885 890 895
20844 Ile Gly Thr Leu Gln Leu Leu Gly Ala Leu Pro Ser Ala Phe Lys Glu
20845 900 905 910
20847 Ala Glu Glu Leu Gly Asn Arg Thr Pro Leu Leu Pro Ile Leu Gly Gln
20848 915 920 925
20850 Leu Glu Glu Val Ala Gly Lys Asn Ile Leu Ser Thr Leu Ala Thr Gly
20851 930 935 940
20853 Arg Asp Ser Thr Leu Asp Thr Ala Cys Ile Asp Gln Ser Thr Val Ala
20854 945 950 955 960
20856 Ile Ala Gly Met Asn Glu Thr Gln Gln Lys Ala Leu Leu Asp Met Phe
20857 965 970 975
20859 Phe Ser Asn Ala Asp Ile Val Pro Gly Pro Leu Met Glu Asp Asn Thr
20860 980 985 990
20862 Arg Leu Met Ala Val Phe Glu Thr Phe Lys Lys Arg Asp Ala Leu Arg
E--> 20863 995 1000 1005
20865 Glu Val Leu Gln Thr Glu Gly Leu Ile Lys Thr Ala Val Glu Leu Leu
E--> 20866 1010 1015 1020
20868 Arg Ala Met Arg Gly Thr Gln Arg Gln Leu Tyr Ser Ser Ala Arg Ile
E--> 20869 1025 1030 1035 1040
20871 Arg Phe Asp Lys Leu Asp Gly Val Asn Thr Asp Asn Pro Glu Asn Met
E--> 20872 1045 1050 1055
20874 Trp Ala Leu Thr Pro Val Val Ser Leu Val Phe Ala Leu Ser Ser Arg
E--> 20875 1060 1065 1070
20877 Leu His Ala His Glu Leu Ile Gly Lys Thr Arg Thr Leu Asp Arg Ala
E--> 20878 1075 1080 1085
20880 Ser Ala Gly Trp Gly Arg Ile Ala Asp Leu Val Pro Asp Leu Val Thr

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Resigned

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 PATENT APPLICATION: US/09/602,874
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Input Set : A:\seqlist.txt
 Output Set : N:\CRF3\07072000\I602874.raw

E--> 20881 1090 1095 1100
 20883 Gly Asp Leu Ile Ser Ala Glu Ala Met Val Leu Gly Ala Arg Asn Pro
 E--> 20884 1105 1110 1115 1120
 20886 Gly Leu Val Asp
 21320 <210> SEQ ID NO: 288
 21321 <211> LENGTH: 1233
 21322 <212> TYPE: PRT
 21323 <213> ORGANISM: Corynebacterium glutamicum
 21325 <400> SEQUENCE: 288
 21326 Val Thr Ile Ser Arg Arg Leu Lys Gln Glu Arg Ser Phe Ala Asp Asp
 21327 1 5 10 15
 21329 Leu Gln Asp Leu Lys Thr Leu Asn Asp Gln Leu Arg Phe Thr Asn Ala
 21330 20 25 30
 21332 Lys Leu Gln Ala Arg Ile Ser Gly Ile Gly Asn Asp Gly Lys Lys Ile
 21333 35 40 45
 21335 Thr Arg Pro Thr Pro Leu Leu Ala Leu Asp Phe Gln Leu Thr Val Glu
 21336 50 55 60
 21338 Glu Tyr Glu Thr Ile Ile Ala Ile Leu Val Glu Ala Val Gly Gly Asn
 21339 65 70 75 80
 21341 Gln Ser Lys Pro Ala Ile Leu Lys Asp Leu Phe Ile Glu Tyr Pro Leu
 21342 85 90 95
 21344 Val Phe Leu Ala Ala Leu Ser Gly Thr Ala Met Leu Asp Ala Gln Glu
 21345 100 105 110
 21347 Gly Phe Trp Pro Ala Phe Trp Lys Arg Thr Gln Val Ser Val Pro Glu
 21348 115 120 125
 21350 His Val Tyr Asp Ala Ile Arg Lys Glu Leu Val Asn Ser Ile Arg Lys
 21351 130 135 140
 21353 Asn Gly Leu Glu Thr Phe Ser Leu Ala Asp Leu Asn Arg Arg Glu Tyr
 21354 145 150 155 160
 21356 Val Gly Leu Ile Gln Leu His Ser Gly Leu Ser Ala Lys Asp Met Leu
 21357 165 170 175
 21359 Ala Leu Val Lys Phe Ile Asp His Thr Arg Ala Glu Asn Gln Gly Trp
 21360 180 185 190
 21362 Asp Ser Gly Glu Asp Phe Ala Ser Tyr Ala Lys Ser Val Phe Ser Ser
 21363 195 200 205
 21365 Gly Asp Asn Leu Leu Thr Thr Glu Ser Leu Lys Gln Leu Val Thr His
 21366 210 215 220
 21368 Ile Pro Ala Arg Ser Val Asp Phe Ile Ala Arg Val Tyr Glu Leu Thr
 21369 225 230 235 240
 21371 Asn Trp Tyr Arg Asp Leu Lys Asp Leu Asn Glu Val Glu Ala Phe Val
 21372 245 250 255
 21374 Gly Thr His Gly Leu Pro Glu Leu Ser Phe Lys Phe Leu Leu Glu Cys
 21375 260 265 270
 21377 Leu Ser Gly Glu Ala Glu Gln Ile Ala Glu Lys Thr Lys Ala Ala Pro
 21378 275 280 285
 21380 Ala Ser Leu Glu Asn Leu Glu Pro Pro His Leu Tyr Leu Asp Pro Gln
 21381 290 295 300
 21383 Ser Phe Glu Leu Ser Leu Val Phe Pro Ala Ile Ser Lys Thr Ala Ala
 21384 305 310 315 320

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Input Set : A:\seqlist.txt

Output Set: N:\CRF3\07072000\I602874.raw

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21386 Leu Gln Ile Pro Ala Pro Glu Trp Thr Val Ile Tyr Asp Gly Asn Ser
21387                               325                               330
21389 Ile Lys Val Arg Pro Glu Gln Asp Trp Ser Tyr Gly Gly Phe Ala Glu
21390                               340                               345
21392 Tyr Arg Leu Pro Leu Asp Lys Pro Leu Ser Ser Leu Arg Val Ile Thr
21393                               355                               360
21395 Pro Thr Glu Lys Ser Leu Ile Leu Ile Glu Gly Phe Gly His Lys Asn
21396                               370                               375
21398 Pro Ile Met Phe Phe Lys Asn Asn Gly Gln Pro Tyr Ala Asn Gln Glu
21399                               385                               390
21401 Met Leu Ser Gly Asn Ala Val Thr Ala Ile Val Pro Ala Ala Ala Ile
21402                               405                               410
21404 Ile Arg Ala Arg Met Arg Ala Ser Lys Thr Phe Asn Tyr Gln Asp Leu
21405                               420                               425
21407 Gly Pro Leu Ser Gly Trp Asn Lys Trp Val Ile Arg Ser Ile Pro Leu
21408                               435                               440
21410 Lys Arg Ala Glu Ser Ile Thr Val Ser His Gly Gly Phe Arg Lys Glu
21411                               450                               455
21413 Leu Pro Val Arg Arg Lys Val Asp Val Gln Trp Ile Thr Glu Asp Leu
21414                               465                               470
21416 Thr Ile Glu Asn Leu Gln Gly Leu Asp His Glu Pro Val Phe His Thr
21417                               485                               490
21419 Ser Pro Arg Ile Glu Phe Pro Thr Ser Gly Ser Asn Trp Val Ile Gln
21420                               500                               505
21422 Tyr Ser Gln Ile Leu Pro Asp Gly Ser Leu Ile Glu Met Glu Asp Tyr
21423                               515                               520
21425 Pro Val Glu Pro Glu Asn Phe Gly Tyr Glu Leu Asp Leu Phe Glu Glu
21426                               530                               535
21428 Ser Asp Asp Pro Trp Val Gly Gln Phe Leu Val Thr Leu Leu Lys Asp
21429                               545                               550
21431 Glu Lys Val Tyr Glu Thr Arg Lys Phe Asn Leu Ala Glu Gly Leu Asp
21432                               565                               570
21434 Leu Ser Leu Thr Phe Ser Gly Gly Gly Pro Glu Asn Arg Phe Arg Tyr
21435                               580                               585
21437 Pro Ser Ile Asn Gln Gly Gln Thr Gly Leu Thr Lys Thr Phe Ala Arg
21438                               595                               600
21440 Phe Ser Ser Asn Ser Glu Lys His Ile Arg Phe Pro Asp Glu Ile Ile
21441                               610                               615
21443 Gly Leu Asp Ala Phe Thr Ser Gln Lys Ala Phe Asn Ile Ala Ser Gly
21444                               625                               630
21446 Asp Phe Pro Glu Asp Tyr Asn Leu Asp Val Phe Ile Thr Pro Pro Gln
21447                               645                               650
21449 Leu His Tyr Gln Val Pro Val Thr His Ser Gln Thr Lys Trp Glu Ser
21450                               660                               665
21452 Thr Lys Thr Thr Leu Asp Phe Asn Asp Phe Ala Asp Gly Asn Leu Gln
21453                               675                               680
21455 Ile Arg Phe Pro Asn Glu Val Tyr Asp Pro Asn Leu Lys Ile Ile Lys
21456                               690                               695
21458 Met Val Ala Tyr Lys Lys Pro Glu Ser Ser Glu Pro Lys Tyr Leu Ser

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Output Set : N:\CRF3\07072000\I602874.raw

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21459 705          710          715          720
21461 Lys Ile Gly Ser Ser Lys Val Trp Ser Ile Pro Met Asp Arg Ile Lys
21462          725          730          735
21464 Glu Leu Met Asp Asp Ala Gln Phe Leu Leu Ile Ala Glu Trp Phe
21465          740          745          750
21467 Ala Glu Ser Lys Asp Gln His Arg Glu Lys Ile Ile Ser Glu Ala Lys
21468          755          760          765
21470 Arg Thr Gly Lys Ile Ser Asn Ala Ala Leu Lys Ser Ala Arg Pro Gln
21471          770          775          780
21473 Pro Gln Ala Ser Ser His Ile Ala Thr Ile Glu Lys Lys Pro Leu Leu
21474 785          790          795          800
21476 Ala Ala Ala Glu Ile Lys Leu Ser Thr Val Glu Leu Glu Leu Gly Arg
21477          805          810          815
21479 His Thr Ser Lys Arg Leu Glu Gly Trp Ala Trp Ser Ala Leu Asn Pro
21480          820          825          830
21482 Leu Asp Pro Pro Ile Lys Val Asp Phe Gln Gly Thr Ser Gly Ser Leu
21483          835          840          845
21485 Pro Asp Thr His Phe Val Val Gly Pro Leu Ile Val Glu Val Arg Glu
21486          850          855          860
21488 Lys Glu Phe Leu Ser Gln Trp Gln Pro Lys Val Pro Ser Val Lys Ala
21489 865          870          875          880
21491 Val Val Ala Asn Asp Pro Ser Phe Glu Leu Asp Pro Gln Phe Asp Pro
21492          885          890          895
21494 Phe Leu Thr His Arg Trp Met Phe Ala Pro Arg Ser Gly Lys Val Leu
21495          900          905          910
21497 Leu Pro Gln Glu Ile Arg Thr Val Trp Asp Ala Arg Phe Asn Met Arg
21498          915          920          925
21500 His Val Leu Ala Gln Arg Glu Asn Leu His Val Lys Ser Ile Gln Asp
21501          930          935          940
21503 Phe Asp Asp Ala Thr Ser Thr Tyr Leu Thr Ser Asp Pro Arg Val Ala
21504 945          950          955          960
21506 Leu Asp Glu Leu Asp Lys Ser Ser Ile Pro Ser Asn Ser His Phe Glu
21507          965          970          975
21509 Ser Phe Ile Arg Ser Gly Leu Ala Glu Leu Ser Phe Glu Val Asp Asp
21510          980          985          990
21512 Thr Ala Gly Asp Ile His Arg Val Pro Trp Ile Gly Leu Ile Gln Glu
E--> 21513 995          1000          1005
21515 Met Asn Asp Leu Arg Ile Leu Gln Ile Gln Gly Tyr Glu Thr Glu Glu
E--> 21516 1010          1015          1020
21518 Arg Ala Ile Glu Arg Arg Asn Ser Gln Ser Tyr Ile Arg Glu Ile Gly
E--> 21519 1025          1030          1035          1040
21521 Gly Ser Glu Leu Trp Asn Ile Leu Lys Gly Asn Ser Glu Gly Leu Ser
E--> 21522          1045          1050          1055
21524 Leu Ala Gln Lys Cys Ala Pro Gln Ala Thr Glu Ile Asn Val Ile Arg
E--> 21525          1060          1065          1070
21527 Asn Ser Gly Leu Glu Ala Met Arg Asn Gly Leu Gly Ala Asp Gln Phe
E--> 21528 1075          1080          1085
21530 Ser Ala Glu Phe Ile Ser Ala Asp Ser Arg Leu Arg Ala Gln Leu Glu
E--> 21531 1090          1095          1100

```

*when amino acid is not
the last one on a line,
begin number under first letter*

RAW SEQUENCE LISTING

DATE: 07/07/2000

PATENT APPLICATION: US/09/602,874

TIME: 13:17:50

Input Set : A:\seqlist.txt

Output Set: N:\CRF3\07072000\I602874.raw

```

21533 Trp Leu Glu Asn Arg Arg Glu Leu Asn Asp Leu Gly Gln Leu Pro Thr
E--> 21534 1105      1110      1115      1120
21536 Leu Phe Asp Phe Ala Glu Lys Tyr Glu Tyr Leu Ile Asp His Leu Gly
E--> 21537      1125      1130      1135
21539 Asp Asp Arg Ile Lys Val Thr Ala Arg Glu Leu Ser Thr Leu Ala Ser
E--> 21540      1140      1145      1150
21542 Glu His Arg Arg Gly Asn Ala Glu Asn Trp Leu Tyr Ala Pro Tyr Val
E--> 21543      1155      1160      1165
21545 Ser Phe Ile Tyr Ser Leu Leu Asn Arg Met Ile Ala His Glu Val Ile
E--> 21546      1170      1175      1180
21548 Arg Pro Ile Ala Gln Ile Asn Tyr Ser Arg His Asp Trp Ala Asn Ala
E--> 21549 1185      1190      1195      1200
21551 Ala Arg Leu Ile Pro Arg Leu Thr Gly Phe Asp Leu Val Ser Ala Glu
E--> 21552      1205      1210      1215
21554 Ala Lys Val Leu Ser Ala Ile Asn Asn Asn Asn Ile Ile Pro Thr Ala
E--> 21555      1220      1225      1230
21557 Ile

```

VERIFICATION SUMMARY DATE: 07/07/2000
PATENT APPLICATION: US/09/602,874 TIME: 13:17:51

Input Set : A:\seqlist.txt
Output Set: N:\CRF3\07072000\I602874.raw

L:8 M:283 W: Missing Blank Line separator, <120> field identifier
L:10 M:283 W: Missing Blank Line separator, <130> field identifier
L:11 M:283 W: Missing Blank Line separator, <140> field identifier
L:12 M:271 C: Current Filing Date differs, Replaced Current Filing Date
L:13 M:283 W: Missing Blank Line separator, <160> field identifier
L:1641 M:351 W: Sequence data Name/Key Feature Out-of-Range, SEQ ID#: 25, CDS LOCATION:12..1583
L:7339 M:351 W: Sequence data Name/Key Feature Out-of-Range, SEQ ID#: 91, CDS LOCATION:37..249
L:8639 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:113
L:8643 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:113
L:8843 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:114
M:332 Repeated in SeqNo=114
L:11802 M:351 W: Sequence data Name/Key Feature Out-of-Range, SEQ ID#: 157, CDS LOCATION:75..332
L:16547 M:351 W: Sequence data Name/Key Feature Out-of-Range, SEQ ID#: 229, CDS LOCATION:19..558
L:20637 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:283
L:20641 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:283
L:20645 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:283
L:20649 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:283
L:20653 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:283
L:20657 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:283
L:20661 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:283
L:20665 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:283
L:20863 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:284
M:332 Repeated in SeqNo=284
L:21259 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:287
L:21263 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:287
L:21267 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:287
L:21271 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:287
L:21275 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:287
L:21279 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:287
L:21283 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:287
L:21287 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:287
L:21291 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:287
L:21295 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:287
L:21299 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:287
L:21303 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:287
L:21307 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:287
L:21311 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:287
L:21513 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:288
M:332 Repeated in SeqNo=288